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TABLE 1
Prevention/Reduction of Proteinuria by Treatment
With Anti-C5 Antibodies

	Before Treatment	After Treatment
	Urine Protein (mg/dL)	Urine Protein (mg/dL)

FBS Control

mouse A	none	100
mouse B	none	500
mouse C	none	500
mouse D*	trace	trace
mouse E	100	100

Anti-C5 Treated

mouse 1	none	none
mouse 2	none	30
mouse 3	30	trace
mouse 4	30	30
mouse 5	30	30
mouse 6	100	30

* Mouse D had more than 500mg/dL urine glucose after treatment

2189015

WO 95/29697

PCT/US95/05688

- 80 -

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Evans, Mark J.
Matis, Louis A.
Mueller, Eileen Elliott
Nye, Steven H.
Rollins, Scott
Rother, Russell P..
Springhorn, Jeremy P.
Squinto, Stephen P.
Thomas, Thomas C.
Wang, Yi
Wilkins, James A.

(ii) TITLE OF INVENTION: METHOD AND COMPOSITIONS FOR THE TREATMENT
OF GLOMERULONEPHRITIS AND OTHER INFLAMMATORY DISEASES

(iii) NUMBER OF SEQUENCES: 19

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Maurice M. Klee
(B) STREET: 1951 Burr Street
(C) CITY: Fairfield
(D) STATE: Connecticut
(E) COUNTRY: USA
(F) ZIP: 06430

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: 3.5 inch, 1.4Mb storage
(B) COMPUTER: Macintosh Cetris 610
(C) OPERATING SYSTEM: System 7
(D) SOFTWARE: WordPerfect 3.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

- 81 -

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/236,208
(B) FILING DATE: 02-MAY-1994

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Klee, Maurice M.
(B) REGISTRATION NUMBER: 30,399
(C) REFERENCE/DOCKET NUMBER: ALX-138
(ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (203) 255-1400
(B) TELEFAX: (203) 254-1101

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
(B) TYPE: Amino Acid
(C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(A) DESCRIPTION: KSSKC peptide

(iii) HYPOTHETICAL: No

(iv) ANTI-SENSE: No

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Val Ile Asp His Gln Gly Thr Lys Ser Ser ...
5 10

Lys Cys Val Arg Gln Lys Val Glu Gly Ser Ser
15 20

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1658 Amino Acids
(B) TYPE: Amino Acid

- (C) STRANDEDNESS: Single
(D) TOPOLOGY: Linear
(A) DESCRIPTION: Pro-C5 Polypeptide
(iii) HYPOTHETICAL: No
(iv) ANTIISENSE: No
(vi) ORIGINAL SOURCE:
(A) ORGANISM: Homo sapiens
(x) PUBLICATION INFORMATION:
(A) AUTHORS: Haviland, D.L.
Haviland, J.C.
Fleischer, D.T.
Hunt, A.
Wetsel, R.A.
(B) TITLE: Complete cDNA Sequence of Human
Complement Pro-C5
(C) JOURNAL: Journal of Immunology
(D) VOLUME: 146
(F) PAGES: 362-368
(G) DATE: 1991

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Leu Leu Gly Ile Leu Cys Phe Leu
-15 -10

Ile Phe Leu Gly Lys Thr Trp Gly Gln Glu Gln Thr Tyr Val
-5 -1 5

Ile Ser Ala Pro Lys Ile Phe Arg Val Gly Ala Ser Glu Asn
10 15 20

Ile Val Ile Gln Val Tyr Gly Tyr Thr Glu Ala Phe Asp Ala
25 30

Thr Ile Ser Ile Lys Ser Tyr Pro Asp Lys Lys Phe Ser Tyr

- 83 -

35		40		45
Ser Ser Gly His Val His Leu Ser Ser Glu Asn Lys Phe Gln				
50		55		60
Asn Ser Ala Ile Leu Thr Ile Gln Pro Lys Gln Leu Pro Gly				
65		70		75
Gly Gln Asn Pro Val Ser Tyr Val Tyr Leu Glu Val Val Ser				
80		85		90
Lys His Phe Ser Lys Ser Lys Arg Met Pro Ile Thr Tyr Asp				
95		100		
Asn Gly Phe Leu Phe Ile His Thr Asp Lys Pro Val Tyr Thr				
105		110		115
Pro Asp Gln Ser Val Lys Val Arg Val Tyr Ser Leu Asn Asp				
120		125		130
Asp Leu Lys Pro Ala Lys Arg Glu Thr Val Leu Thr Phe Ile				
135		140		145
Asp Pro Glu Gly Ser Glu Val Asp Met Val Glu Glu Ile Asp				
150		155		160
His Ile Gly Ile Ile Ser Phe Pro Asp Phe Lys Ile Pro Ser				
165		170		
Asn Pro Arg Tyr Gly Met Trp Thr Ile Lys Ala Lys Tyr Lys				
175		180		185
Glu Asp Phe Ser Thr Thr Gly Thr Ala Tyr Phe Glu Val Lys				
190		195		200
Glu Tyr Val Leu Pro His Phe Ser Val Ser Ile Glu Pro Glu				
205		210		215

Tyr Asn Phe Ile Gly Tyr Lys Asn Phe Lys Asn Phe Glu Ile
220 225 230

Thr Ile Lys Ala Arg Tyr Phe Tyr Asn Lys Val Val Thr Glu
235 240

Ala Asp Val Tyr Ile Thr Phe Gly Ile Arg Glu Asp Leu Lys
245 250 255

Asp Asp Gln Lys Glu Met Met Gln Thr Ala Met Gln Asn Thr
260 265 270

Met Leu Ile Asn Gly Ile Ala Gln Val Thr Phe Asp Ser Glu
275 280 285

Thr Ala Val Lys Glu Leu Ser Tyr Tyr Ser Leu Glu Asp Leu
290 295 300

Asn Asn Lys Tyr Leu Tyr Ile Ala Val Thr Val Ile Glu Ser
305 310

Thr Gly Gly Phe Ser Glu Glu Ala Glu Ile Pro Gly Ile Lys
315 320 325

Tyr Val Leu Ser Pro Tyr Lys Leu Asn Leu Val Ala Thr Pro
330 335 340

Leu Phe Leu Lys Pro Gly Ile Pro Tyr Pro Ile Lys Val Gln
345 350 355

Val Lys Asp Ser Leu Asp Gln Leu Val Gly Gly Val Pro Val
360 365 370

Ile Leu Asn Ala Gln Thr Ile Asp Val Asn Gln Glu Thr Ser
375 380

Asp Leu Asp Pro Ser Lys Ser Val Thr Arg Val Asp Asp Gly
385 390 395

2189015

Val Ala Ser Phe Val Leu Asn Leu Pro Ser Gly Val Thr Val
400 405 410

Leu Glu Phe Asn Val Lys Thr Asp Ala Pro Asp Leu Pro Glu
415 420 425

Glu Asn Gln Ala Arg Glu Gly Tyr Arg Ala Ile Ala Tyr Ser
430 435 440

Ser Leu Ser Gln Ser Tyr Leu Tyr Ile Asp Trp Thr Asp Asn
445 450

His Lys Ala Leu Leu Val Gly Glu His Leu Asn Ile Ile Val
455 460 465

Thr Pro Lys Ser Pro Tyr Ile Asp Lys Ile Thr His Tyr Asn
470 475 480

Tyr Leu Ile Leu Ser Lys Gly Lys Ile Ile His Phe Gly Thr
485 490 495

Arg Glu Lys Phe Ser Asp Ala Ser Tyr Gln Ser Ile Asn Ile
500 505 510

Pro Val Thr Gln Asn Met Val Pro Ser Ser Arg Leu Leu Val
515 520

Tyr Tyr Ile Val Thr Gly Glu Gln Thr Ala Glu Leu Val Ser
525 530 535

Asp Ser Val Trp Leu Asn Ile Glu Glu Lys Cys Gly Asn Gln
540 545 550

Leu Gln Val His Leu Ser Pro Asp Ala Ala Tyr Ser Pro
555 560 565

Gly Gln Thr Val Ser Leu Asn Met Ala Thr Gly Met Asp Ser
570 575 580

Trp Val Ala Leu Ala Ala Val Asp Ser Ala Val Tyr Gly Val
585 590

Gln Arg Gly Ala Lys Lys Pro Leu Glu Arg Val Phe Gln Phe
595 600 605

Leu Glu Lys Ser Asp Leu Gly Cys Gly Ala Gly Gly Gly Leu
610 615 620

Asn Asn Ala Asn Val Phe His Leu Ala Gly Leu Thr Phe Leu
625 630 635

Thr Asn Ala Asn Ala Asp Asp Ser Gln Glu Asn Asp Glu Pro
640 645 650

Cys Lys Glu Ile Leu Arg Pro Arg Arg Thr Leu Gln Lys Lys
655 660

Ile Glu Glu Ile Ala Ala Lys Tyr Lys His Ser Val Val Lys
665 670 675

Lys Cys Cys Tyr Asp Gly Ala Cys Val Asn Asn Asp Glu Thr
680 685 690

Cys Glu Gln Arg Ala Ala Arg Ile Ser Leu Gly Pro Arg Cys
695 700 705

Ile Lys Ala Phe Thr Glu Cys Cys Val Val Ala Ser Gln Leu
710 715 720

Arg Ala Asn Ile Ser His Lys Asp Met Gln Leu Gly Arg Leu
725 730

His Met Lys Thr Leu Leu Pro Val Ser Lys Pro Glu Ile Arg
735 740 745

Ser Tyr Phe Pro Glu Ser Trp Leu Trp Glu Val His Leu Val
750 755 760

Pro Arg Arg Lys Gln Leu Gln Phe Ala Leu Pro Asp Ser Leu
765 770 775

Thr Thr Trp Glu Ile Gln Gly Ile Gly Ile Ser Asn Thr Gly
780 785 790

Ile Cys Val Ala Asp Thr Val Lys Ala Lys Val Phe Lys Asp
795 800

Val Phe Leu Glu Met Asn Ile Pro Tyr Ser Val Val Arg Gly
805 810 815

Glu Gln Ile Gln Leu Lys Gly Thr Val Tyr Asn Tyr Arg Thr
820 825 830

Ser Gly Met Gln Phe Cys Val Lys Met Ser Ala Val Glu Gly
835 840 845

Ile Cys Thr Ser Glu Ser Pro Val Ile Asp His Gln Gly Thr
850 855 860

Lys Ser Ser Lys Cys Val Arg Gln Lys Val Glu Gly Ser Ser
865 870

Ser His Leu Val Thr Phe Thr Val Leu Pro Leu Glu Ile Gly
875 880 885

Leu His Asn Ile Asn Phe Ser Leu Glu Thr Trp Phe Gly Lys
890 895 900

Glu Ile Leu Val Lys Thr Leu Arg Val Val Pro Glu Gly Val
905 910 915

- 88 -

Lys Arg Glu Ser Tyr Ser Gly Val Thr Leu Asp Pro Arg Gly
 920 925 930

Ile Tyr Gly Thr Ile Ser Arg Arg Lys Glu Phe Pro Tyr Arg
 935 940

Ile Pro Leu Asp Leu Val Pro Lys Thr Glu Ile Lys Arg Ile
 945 950 955

Leu Ser Val Lys Gly Leu Leu Val Gly Glu Ile Leu Ser Ala
 960 965 970

Val Leu Ser Gln Glu Gly Ile Asn Ile Leu Thr His Leu Pro
 975 980 985

Lys Gly Ser Ala Glu Ala Glu Leu Met Ser Val Val Pro Val
 990 995 1000

Phe Tyr Val Phe His Tyr Leu Glu Thr Gly Asn His Trp Asn
 1005 1010

Ile Phe His Ser Asp Pro Leu Ile Glu Lys Gln Lys Leu Lys
 1015 1020 1025

Lys Lys Leu Lys Glu Gly Met Leu Ser Ile Met Ser Tyr Arg
 1030 1035 1040

Asn Ala Asp Tyr Ser Tyr Ser Val Trp Lys Gly Gly Ser Ala
 1045 1050 1055

Ser Thr Trp Leu Thr Ala Phe Ala Leu Arg Val Leu Gly Gln
 1060 1065 1070

Val Asn Lys Tyr Val Glu Gln Asn Gln Asn Ser Ile Cys Asn
 1075 1080

Ser Leu Leu Trp Leu Val Glu Asn Tyr Gln Leu Asp Asn Gly
 1085 1090 1095

Ser Phe Lys Glu Asn Ser Gln Tyr Gln Pro Ile Lys Leu Gln
 1100 1105 1110

Gly Thr Leu Pro Val Glu Ala Arg Glu Asn Ser Leu Tyr Leu
 1115 1120 1125

Thr Ala Phe Thr Val Ile Gly Ile Arg Lys Ala Phe Asp Ile
 1130 1135 1140

Cys Pro Leu Val Lys Ile Asp Thr Ala Leu Ile Lys Ala Asp
 1145 1150

Asn Phe Leu Leu Glu Asn Thr Leu Pro Ala Gln Ser Thr Phe
 1155 1160 1165

Thr Leu Ala Ile Ser Ala Tyr Ala Leu Ser Leu Gly Asp Lys
 1170 1175 1180

Thr His Pro Gln Phe Arg Ser Ile Val Ser Ala Leu Lys Arg
 1185 1190 1195

Glu Ala Leu Val Lys Gly Asn Pro Pro Ile Tyr Arg Phe Trp
 1200 1205 1210

Lys Asp Asn Leu Gln His Lys Asp Ser Ser Val Pro Asn Thr
 1215 1220

Gly Thr Ala Arg Met Val Glu Thr Thr Ala Tyr Ala Leu Leu
 1225 1230 1235

Thr Ser Leu Asn Leu Lys Asp Ile Asn Tyr Val Asn Pro Val
 1240 1245 1250

Ile Lys Trp Leu Ser Glu Glu Gln Arg Tyr Gly Gly Gly Phe
 1255 1260 1265

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WO 95/29697

PCT/US95/05688

-- 90 --

Tyr Ser Thr Gln Asp Thr Ile Asn Ala Ile Glu Gly Leu Thr
 1270 1275 1280

Glu Tyr Ser Leu Leu Val Lys Gln Leu Arg Leu Ser Met Asp
 1285 1290

Ile Asp Val Ser Tyr Lys His Lys Gly Ala Leu His Asn Tyr
 1295 1300 1305

Lys Met Thr Asp Lys Asn Phe Leu Gly Arg Pro Val Glu Val
 1310 1315 1320

Leu Leu Asn Asp Asp Leu Ile Val Ser Thr Gly Phe Gly Ser
 1325 1330 1335

Gly Leu Ala Thr Val His Val Thr Thr Val Val His Lys Thr
 1340 1345 1350

Ser Thr Ser Glu Glu Val Cys Ser Phe Tyr Leu Lys Ile Asp
 1355 1360

Thr Gln Asp Ile Glu Ala Ser His Tyr Arg Gly Tyr Gly Asn
 1365 1370 1375

Ser Asp Tyr Lys Arg Ile Val Ala Cys Ala Ser Tyr Lys Pro
 1380 1385 1390

Ser Arg Glu Glu Ser Ser Ser Gly Ser Ser His Ala Val Met
 1395 1400 1405

Asp Ile Ser Leu Pro Thr Gly Ile Ser Ala Asn Glu Glu Asp
 1410 1415 1420

Leu Lys Ala Leu Val Glu Gly Val Asp Gln Leu Phe Thr Asp
 1425 1430

Tyr Gln Ile Lys Asp Gly His Val Ile Leu Gln Leu Asn Ser
 1435 1440 1445

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Ile Pro Ser Ser Asp Phe Leu Cys Val Arg Phe Arg Ile Phe
1450 1455 1460

Glu Leu Phe Glu Val Gly Phe Leu Ser Pro Ala Thr Phe Thr
1465 1470 1475

Val Tyr Glu Tyr His Arg Pro Asp Lys Gln Cys Thr Met Phe
1480 1485 1490

Tyr Ser Thr Ser Asn Ile Lys Ile Gln Lys Val Cys Glu Gly
1495 1500

Ala Ala Cys Lys Cys Val Glu Ala Asp Cys Gly Gln Met Gln
1505 1510 1515

Glu Glu Leu Asp Leu Thr Ile Ser Ala Glu Thr Arg Lys Gln
1520 1525 1530

Thr Ala Cys Lys Pro Glu Ile Ala Tyr Ala Tyr Lys Val Ser
1535 1540 1545

Ile Thr Ser Ile Thr Val Glu Asn Val Phe Val Lys Tyr Lys
1550 1555 1560

Ala Thr Leu Leu Asp Ile Tyr Lys Thr Gly Glu Ala Val Ala
1565 1570

Glu Lys Asp Ser Glu Ile Thr Phe Ile Lys Lys Val Thr Cys
1575 1580 1585

Thr Asn Ala Glu Leu Val Lys Gly Arg Gln Tyr Leu Ile Met
1590 1595 1600

Gly Lys Glu Ala Leu Gln Ile Lys Tyr Asn Phe Ser Phe Arg
1605 1610 1615

Tyr Ile Tyr Pro Leu Asp Ser Leu Thr Trp Ile Glu Tyr Trp
1620 1625 1630

Pro Arg Asp Thr Thr Cys Ser Ser Cys Gln Ala Phe Leu Ala
1635 1640 1645

Asn Leu Asp Glu Phe Ala Glu Asp Ile Phe Leu Asn Gly Cys
1645 1650 1655

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 4059 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: Circular

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: Apex-1 Eukaryotic
Expression Vector

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACGGCTTGAC ATTGATTATT GACTAGTTAT TAATAGTAAT CAATTACGGG 50
GTCATTAGTT CATAGCCCAT ATATGGAGTT CCGCGTTACA TAACCTACGG 100
TAAATGGCCC CGCCTGGCTG ACCGCCCCAC GACCCCGGCC CATTGACGTC 150
AATAATGAAG TATGTTCCCA TAGTAACGCC AATAGGAGT TTCCATTGAC 200
GTCAATGGGT GGACTATTTA CGGTAACCTG CCCACTTGCC AGTACATCAA 250
GTGTATCATA TGCCAAAGTAC GCCCCCTATT GACGTCAATG ACGGTAAATG 300
GCCCGCCTGG CATTATGCCC AGTACATGAC CTTATGGGAC TTTCCTACTT 350
GCCAGTACAT CTACGTATTA GTCATCGCTA TTACCAATGT GATCGCGTTT 400

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TGGCAGTACA TCAATGGGCG TGGATAGCGG TTTGACTCAC GGGGATTTC 450
 AAGTCTCCAC CCCATTGACG TCAATGGGAG TTTGTTTTGG CACCAAAATC 500
 AACGGGACTT TCCAAATGT COTAAACAAT CCCCCCCTT GACGCAATG 550
 GCGGGTAGGC GTGTACGGTG GGAGGTCTAT ATAAGCAGAG CTCGTTTAGT 600
 GAACCGTCAG AATTCTGTTG GGCTCGCGGT TGATTACAAA CTCCTGCGG 650
 TCTTTCAGT ACTCTGGAT CGGAACCCG TCGGCTCCG AACGGTACTC 700
 CGCCACCGAG GGACCTGACG GAGTCGCGAT CGACCGGATC GGAAGACCTC 750
 TCGACTGTG GGGTGAGTAC TCCCTCTCAA AAGCGGGCAT GACTTCTGG 800
 CTAAGATTGT CAGTTTCCAA AAACGAGGAG GATTGATAT TCACTGGCC 850
 CGCGGTGATG CCTTTGAGGG TGGCCGCTC CATCTGGTCA GAAAGACAA 900
 TCTTTTGTG GTCAAGCTTG AGGTGTGGCA GGCTTGAGAT CTGGCCATAC 950
 ACTTGAGTGA CAATGACATC CACTTTGCTT TTCTCTCCAC AGGTGTCCAC 1000
 TCCAGGTCC AATGCAGGT CGACCGGCTT GGTACCGAGC TCGATCCAC 1050
 TAGTAACGGC CGCCAGTGTG CTGGAATTCT GCAGATATCC ATCACACTGG 1100
 CGGCCGCTCG AGCATGCATC TAGAACTTGT TTATTGCAGC TTATAATGGT 1150
 TACAAATAAA GCAATAGCAT CACAAATTC ACAAAATAG CATTTTTTTC 1200
 ACTGCATTCT AGTTGTGGTE TGTCCAACT CATCAATGA TCTTATCATG 1250
 TCTGGATCGA TCCCGCCATG GTATCAACGC CATATTCTTA TTTACAGTAG 1300
 GGACCTCTTC GTTGTGTAGG TACCGCTGTA TTCTAGGGA AATAGTAGAG 1350

GCACCTTGAA CTGTCTGCAT CAGCCATATA GCCCCGCTG TCGACTTAC 1400
 AAACACAGGC ACGTACTGA CAAACCCATA CACCTCCTCT.GAAATACCCA 1450
 TAGTTGCTAG GGCTGTCTCC GAACTCATTA CACCCGCCAA AGTCAGAGCT 1500
 GTAATTTCGC CATCAAGGC AGCGAGGCT TCTCAGATA.AATAGCTTC 1550
 TGCCGAGAGT CCCGTAAGG TAGACACTTC AGCTAATCCC TCGATGAGST 1600
 CTACTAGAAT AGTCAGTGG GCTCCCATTT TGAAATTC ATTACTTGAT 1650
 CAGCTTCAGA AGATGGCGGA GGGCCTCCAA CACAGTAATT TTCTCCCGA 1700
 CTCTTAAAT AGAAATGTC AAGTCAGTTA AGCAGGAAGT GGACTAACTG 1750
 ACGCAGCTGG CCGTGCAGCA TCCTCTTTTA ATTAGTTGCT AGGCAACGCC 1800
 CTCCAGAGGG CGTGTGTTTT TGCAAGAGGA AGCAAAAGCC TCTCCACCA 1850
 GGCTTAGAAT GTTCCACCC AATCATTACT ATGACAACAG CTGTTTTTTT 1900
 TAGTATTAG CAGAGGCCGG GGAACCCCTGG GCCCGCTTAC TCTGGAGAA 1950
 AAGAAGAGAG GCATTGTAGA GGCTCCAGA GGCAACTTGT CAAAACAGGA 2000
 CNGCTTCTAT TTCTGTCACA CTGTCTGGCC CTGTCACAAG GTCCAGCAC 2050
 TCATACCCC CTTTAAATAG.CAGTTGGGA ACGGGTGCGG GTCTTACTCC 2100
 GCCCATCCG CCCCTAAGTC CGCCAGGTC CGCCATCTT CGGCCCATG 2150
 GCTGACTAAT TTTTTTATT TATGCAGAGG CGAGGCCGC CTGGGCTCT 2200
 GAGCTATTCC AGAAGTAGTG AGGAGGCTTT TTGGAGGCC TAGGCTTTG 2250
 CAAAAAGGAG CTCCAGCAA AAGGCCAGGA ATCGTAAAA GGCCGCGTTG 2300

CTGGCGTTTT TCATAGGCT CCGCCCCCT GACGAGCATC AAAAAATCG 2350

ACGCTCAAGT CAGAGGTGGC GAAACCCGAC AGGACTATAA AGATACCAGG 2400

CGTTTCCCC TGGGAAGCTCC CTGCTGCGCT CTCTGTTC GACCTGCGC 2450

CTTACCGGAT ACCTGTCCGC CTTTCTCCCT TCGGGAAGCG TGGGCTTTC 2500

TCAATGCTCA CGCTGTAGGT ATCTCAGTTC GGTGTAGTTC GTTCGCTCCA 2550

AGCTGGGCTG TGTGCACGAA CCCCCCGTTC AGCCCCGACG CTGCGCCTTA 2600

TCCGGTAACT ATCGTCTTGA GTCCAAACCG GTAAGACAG ACTTATCGCC 2650

ACTGGCAGCA GCCACTGGTA ACAGGATTAG CAGAGCGAGG TATGTAGGCG 2700

GTGCTACAGA GTTCTTGAAG TGTGGCCTA ACTACGGCTA CACTAGAAGG 2750

ACAGTATTTG GTATCTGCGC TCTGCTGAAG CCAATTACCT TCGGAAAAAG 2800

AGTTGGTAGC TCTTGATCCG GCAACAAAC CACCGCTGCT AGCGTGGTT 2850

TTTTTGTTFG CAAGCAGCAG ATTACCGCA GAAAAAAGG ATCTCAAGAA 2900

GATCCTTTGA TCTTTCTAC GGGGCTGAC GCTCAGTGA ACGAAAACTC 2950

ACGTTAAGGG ATTTTGGTCA TGAGATTATC AAAAAGGATC TTCACCTAGA 3000

TCCTTTTAAA TAAAAAATGA AGTTTAAAT CAATCTAAAG TATATATGAG 3050

TAACTTGGT CTGACAGTTA CCAATGCTTA ATCAGTGAGG CACCTATCTC 3100

AGCGATCTGT CTATTTCGTT CATCCATAGT TGCTGACTC CCGTCTGT 3150

AGATAACTAC GATACGGGAG GGCCTACCAT TGGCCCCAG TGCTGCAATG 3200

ATACCGCGAG ACCACGCTC ACCGGCTCCA GATTATACG CAATAAACCA 3250

GCCAGCCGGA AGGGCCGAGC GCAGAACTGG TCCTGCAACT TTATCCGCCT 3300
CCATCCAGTC TATTAATTGT TGCCGGGAAG CTAGAGTAAG TAGTTCCGCA 3350
GTTAATAGTT TGCGCAACGT TGTGCCATT GCTACAGGCA TCGTGGTGTC 3400
ACGCTCGTCG TTTGGTATGG CTTCATTGAG CTCGGGTCC CAACGATCAA 3450
GGCGAGTTAC ATGATCCCCC ATGTTGTGCA AAAAAGCGGT TAGCTCCTTC 3500
GGTCCTCCGA TCGTTGTGAG AAGTAAGTGG GCGCAGTGT TATCACTCAT 3550
GGTTATGGCA GCACTGCATA ATTCTCTTAC TGTCAIGCCA TCCGTAAGAT 3600
GCTTTCTGT GACTGGTGAG TACTCAACCA AGTCATTCTG AGAATAGTGT 3650
ATGCGGCGAC CGAGTTGCTC TTGCCCGGCG TCAATACGGG ATAATACCGC 3700
GCCACATAGC AGAAGTTAA AAGTGCTCAT CATGGAAAA CGTTCTTCGG 3750
GGCGAAAACT CTCAGGATC TTACCGCTGT TGAGATCCAG TTGATGTAA 3800
CCCACTGTC CAOCCAACTG ATCTTCAGCA TCTTTEACTT TCACCAGCGT 3850
TTCTGGGTGA GCAAAAACAG GAAGGCAAAA TGCCGCAAAA AAGGGAATAA 3900
GGCGACACG GAAATGTTGA ATACTCATA TCTTCCTTTT TCAATATTAT 3950
TGAAGCATTT ATCAGGGTTA TTGTCTCATG AGCGATACA TATTTGAATG 4000
TATTTAGAAA AATAACAAA TAGGGGTTC GGCACATT CCCCGAAAAG 4050
TGCCACCTG 4059

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(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8540 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Circular

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: Apex-3P Eukaryotic
Expression Vector

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GTGACCAATA CAAAACAAA GCGCCCCCTCG TACCAGCGAA GAAGGGGCAG 50
AGAATGCCGTA GTCAGGTTTA GTTCGTCCCG CGCGGGGGA TCTGTATGGT 100
GCACTCTCAG TACAATCTGC TCTGATGCCG CATAGTTAAG CCAATATCTG 150
CTCCCCTGCTT GTGTGTTGGA GGTCCGCTGAG TAGTGCGCGA GCAAAATTTA 200
AGCTACAACA AGGCAAGGCT TGACCGACAA TTGCATGAAG AATCTGCTTA 250
GGGTTAGGCG TTTTCCGCTG CTTCCGATG TACGGGCCAG ATATACGCGT 300
TGACATTGAT TATTGACTAG TTATTANTAG TAATCAATTA CGGGGTCAAT 350
AGTTCATAGC CCATATATGG AGTTCGCGT TACATRACTT ACGGTAAATG 400
GCCCGCCCTG CTGACCGCCC AACGACCCCC GCCCATTTGAC GTCAATATG 450
ACGTATGTTC CCATAGTAAC GCCAATAGG ACTTTCCATT GACGTCAATG 500
GGTGGACTAT TTACGGTAAA CTGCCACTT GGCAGTACAT CAAGTGTATC 550
ATATGCCAAG TACGCCCCCT ATTGACGTCA ATGACGGTAA ATGGCCCGCC 600
TGGCAATATG CCCAGTACAT GACCTTATG GACTTTCCTA CTTGGCAGTA 650

CATCTACGTA TTATGTCATCG CTATTACCAT GGTGATGCGG TTTTGGCAGT ..700
ACATCAATGG GCGTGGATAG CCGTTTGACT CACGGGGMTT TCCAAGTCTC ...750
CACCCCAATG ACGTCAATGG GAGTTTGTTC TGGCACAAA ATCAACGGGA :800
CTTCCAAAA TGTCGTAACA ACTCGCCCC ATTGACGCAA ATGGGCGGTA .850
GCGGTGTACG GTGGGAGGTC TATATAAGCA GAGCTCGTTT AGTGAACCGT ..900
CAGAACTCTG TTGGGCTCGC GGTTGATTAC AAACCTCTCG CGGTCTTTCC ...950
AGTACTCTTG GATCGGAAC CCGTCGGCCT CCGAACGTA CTCGCCACC 1000
GAGGGACCTG AGCGAGTCCG CATCGACCGG ATCGGAAC CTCTGACTG 1050
TTGGGGTGAG TACTCCCTCT CAAAAGCGG CATGACTTCT GCGCTAAGAT 1100
TGTCACTTC CAAAAACGAG GAGGATTTGA TATTCACCTG GCGCGGGTG 1150
ATGCCCTTGA GGGTGGCGC GTCCATCTGG TCAGAAAAGA CAATCTTTTT 1200
GTTGTCAAGC TTGAGGTGTG GCAGGCTTGA GATCTGGCCA TACACTTGAG 1250
TGACAATGAC ATCCACTTG CCTTCTCTC CACAGGTGTC CACTCCAGG 1300
TCCAATGCA GGTGACCGG CTGTGTACCG AGCTCGGATC CTCTAGATC 1350
GACCTGCAGG CATGCAAGCT TGGCACTGC CGTCGTTTA CAACGTCGTG 1400
ACTGGGAAA CCCTGGCGTT ACCCAACTTA ATCGCCTTGC AGCAGTCCC 1450
CCTTCGCCA GCTGGCGTAA TAGCGAAGG GCCGCAACG ATCCAGACAT 1500
GATAAGATAC ATTGATGAGT TTGGACAAAC CACAAC TAGA ATGCAGTGAA 1550
AAAAATGCTT TATTGTGAA ATTGTGATG CTATTGCTTT ATTGTAAAC 1600

ATTATAAGCT GCAATAACA AGTTAACAC AACAAATGCA TTCAITTTAT 1650
GTTTCAGGTT CAGGGGGAGG TGTGGGAGGT TTTTAAAGC AAGTAAACC 1700
TCTACAAATG TGGTATGGCT GATTATGATC CCCAGGAAGC TCCTCTGTGT 1750
CCTCATAAAC CCTAACCTCC TCTACTTGAG AGGACATTCC AATCATAGGC 1800
TGCCCATCCA CCTCTGTGT CCTCTGTTA ATTAGGTCAC TTAACAAAAA 1850
GGAAATGGG TAGGGGTTT TCACAGACCG CTTCTAAGG GTAAITTTAA 1900
AATATCTGGG AAGTCCCTTC CACTGCTGTG TTCCAGAAGT GTTGGTAAAC 1950
AGCCCAAAA TGTCAACAGC AGAAACATAC AAGCTGTGAG CTTCGCACAA 2000
GGGCCCAACA CCTGCTCAT CAAGAAGCAC TGTGGTGTCT GTGTAGTAA 2050
TGTGCAAAAC AGGAGGCACA TTTTCCCCAC CTGTGTAGGT TCCAAAATAT 2100
CTAGTGTTTT CATTTTACT TGGATCAGGA ACCCAGCACT CCACCTGGATA 2150
AGCATTTTCC TTATCCAAAA CAGCCTGTGT GTCAGTGTC ATCTGCTGAC 2200
TGTCAACTGT AGCATTTTTT GGGGTACAG TTTGAGCAGG ATATTGGTC 2250
CTGTAGTTTG CTAACACACC CTGCAGCTCC AAAGGTCCC CACCAACAGC 2300
AAAAAAATGA AAATTTGACC CTTGAAATGG TTTTCCAGCA CCATTTTCAT 2350
GAGTTTTTTG TGTCCCTGAA TGCAAGTTTA ACATAGCAGT TACCCCAATA 2400
ACCTCAGTTT TAACAGTAAC AGCTTCCCAC ATCAAAATAT TTCCACAGGT 2450
TAAGTCTCTA TTTGTAGAA TCGCCAGCAC AGTGGTCGAC CCTGTGGATG 2500
TGTGTCACTT AGGGTGTGGA AAGTCCCCAG GCTCCCCAGC AGGCAGAAAT 2550

ATGCAAAACA TGCACTCAA TTAGTCAGCA ACCAGGTGTG GAAAGTCCCC 2600
AGGCTCCCCA GCAGGCAGAA GTATGCAAG CATGCATCTC AATTAGTCAG 2650
CAACCTAGT CCGCCCCCTA ACTCCGCCA TCCGCCCCCT AACTCCGCC 2700
AGTCCGCC ATTCCTCGCC CCATGGCTGA CTAATTTTTT TTATTTATGC 2750
AGAGGCCGAG GCGGCTCGG CCTCTAGCT ATTCCAGAAG TAGTGAGGAG 2800
GCTTTTTTGG AGGCCTAGGC TTTTGCAGAA GCTTACCATG ACCGAGTACA 2850
AGCCACCGGT GCGCCTCGCC ACCCGGAGC ACSTCCCCCG GGCCTTACGC 2900
ACCTCTGCGG CCGGTTGCG CGACTACCCC GCCACGGGCC ACACCGTGA 2950
CCCGGACGC CACATCGAGC GGGTCACGA GTGCAAGAA CTCTTCTCA 3000
CGCGCTCGG GCTCGACATC GCGAAGGTGT GGTCTGGGGA CGACGGCGCC 3050
GCGTGGCGG TCTGGACCAC GCGGAGAGC GTCGAAGCGG GGGCGGTGT 3100
CGCCGAGATC GGCCTGGCA TGGCCGAGTT GAGCGGTTC CCGTGGCGG 3150
CGCAGCAACA GATGGAAGGC CTCCTGGCG CGCACCGGCC CAAGGAGCCC 3200
GCGTGTTC TGGCCACCGT CCGGCTCTG CCGGACGACC AGGGCAAGGG 3250
TCTGGGCAG GCGTGTGTC TCCCCGAGT GGAGCGGCC GAGCGCGCC 3300
GGGTGCGCG CTCTCTGGAG ACCTCGGCG CCGCAACTC CCGTTCTAC 3350
GAGCGGCTG GCTTACCGT CACGCGGAC GTGAGTGCC CGAAGGACG 3400
CGGACCTG TGCTGACCC GCAAGCCCG TGGCTGACGC CCGCCCCAG 3450
ACCGCAGCG CCGACCGAA AGGAGGCGAC GACCCCATC ATCGATAAAA 3500

2189015

TAAAGATT TATTAGTCT CCAGAAAAG GGGGAATGA AAGACCCAC 3550
CTGTAGGTTT GGCAAGCTAG AACTTGTTTA TTGCAGCTTA TAATGGTTAC 3600
AAATAAGCA ATAGCATCAC AATTTTACA AATAAGCAT TTTTTCAC 3650
GCATTC TAGT TGTGTTTGT CCAACTCAT CAATGATCT TATCATGTCT 3700
GGATCGATCC CGCCATGTA TCAAGCCAT ATTCTATT ACAGTAGGA 3750
CCTCTCGTT GTGTAGGTAC CCGGGTTCG AATCGAATT CGCCATGAC 3800
AAGACGCTGG GCGGGTTTG TGTCACTATA GAACTAAAG CATGCAATA 3850
TATTTCTTC GGGGACACG CCAGCAACG CGAGCAACG GCCACGGGA 3900
TGAAGCAGCC CGCGGCAC TCCTAAAGG ATTCACACT CCAAGATTG 3950
GAGCCAATCA ATTCTTGGG AAGACTGTA ATCGCAAC CAACCTTGG 4000
CAGACATAT CCATGCGTC CGCATCTCC AGCAGCGCA CGCGCGCAT 4050
CTCGGGCGG ACGCGCTGG CTACGTCTTG CTGCGCTCG CGACGCGAG 4100
CTGGATGGCC TTCCCATTA TGATTCCTCT CGCTTCGGC GGATCGGGA 4150
TGCCCGGTT GCAGGCCATG CTGTCCAGG AGGTAGATGA CGACCATCAG 4200
GGACAGCTTC AAGGATGCT CGCGCTCTT ACCAGGCCA GCAAAAGGC 4250
AGGAACCGTA AAAAGGCGC GTTGCTGGG TTTTCCATA GGCTCCGCC 4300
CCCTGACGAG CATCAGAAA ATCGACGCT AAGTCAGAG TGGCGAACC 4350
CGACAGGACT ATAAAGATAC CAGGCGTTT CCCTCGAAG CTCCCTGTT 4400
CGCTCTCTG TTCCGACCT GCGCTTAC GGATACTGT CCGCTTCTT 4450

CCCTCGGGA AGCGTGGCG TTTCATAG CTCACGCTGT AGGTATCTCA 4500
GTTGCGTGTA GGTGTTCCG TCCAAGCTGG GCTGTGTGCA CGAACCCCC 4550
GTTACAGCCG ACCGCTGGC CTTATCCGT AACTATGTC TTGAGTCCAA 4600
CCCGGTAGA CAGACTAT CGCCACTGC AGCAGCCACT GGTACAGGA 4650
TTAGCAGAGC GAGGTATGA GCGGTGCTA CAGAGTTCTT GAAGTGGTG 4700
CCTAATCAG GCTACACTAG AAGGACAGTA TTTGGTATCT GCGCTCTGCT 4750
GAAGCCAGTT ACCTCGGAA AAGAGTTGG TAGCTCTGA TCCGGCAAC 4800
AAACCACCG TGTAGCGGT GTTTTTTTTT TTGCAAGCA GCAGATTACG 4850
CGCAGAAAAA AAGGATCTCA AGAAGATCTT TTGATCTTT CTACGGGTC 4900
TGACGCTCG TGAACGAAA ACTCAGTTA AGGGATTTTG GTCATGAGAT 4950
TATCAAAAAG GATCTTCACC TAGATCCTTT TAAATTAAAA ATGAAGTTT 5000
AATCAATCT AAGTATATA TGAGTAAAT TGCTCTGACA GTTACCAATG 5050
CTTAATCAGT GAGGCACCTA TCTCAGCAT CTGCTATTT CGTTCATCCA 5100
TAGTTGCTG ACTCCCCGC GTGTAGATA CTAAGATACG GAGGGCTTA 5150
CCATCTGGCC CCAGTCTGC AATGATACCG CGAGACCCAC GCTCACCGC 5200
TCCAGATTA TCAGCAATA ACCAGCCAGC CGAAGGCC GAGCCAGAA 5250
GTGCTCTGC AACTTTATCC GCCTCCATCC AGCTATTAA TTGTTGCCG 5300
GAAGCTAGG TAAGTAGTTC GCCATTAAT AGTTGCGCA ACOTTTGTC 5350
CATTGCTGCA GGCATGCTG TGTACGCTC GTGTTTGGT ATGGCTTCAT 5400

TCAGCTCCGG TTCCAAAGCA TCAAGGCGAG TTACATGATC CCCCATGTTG 5450
TGCAAAAAG CGGTTAGCTC CTTCGGTCCCT CCGATCGTTG TCAGAAGTAA 5500
GTTGGCCGCA GTGTTATCAC TCATGOTTAT GGCAGCACTG CATAAATTCTC 5550
TTACTGTCTAT GCCATCOGTA AGATGCTTTT CTGTGACTGG TGAGTACTCA 5600
ACCAAGTCAT TCTGAGAATA GTGTATGCGG CGACCGAGTT GCTCTTGCCC 5650
GGCGTCAACA CGGGATAATA CCGCGCCACA TAGCAGAACT TTAJJAAGTGC 5700
TCATCATTTGG AAAACGTTCT TCGGGGCGAA AACTCTCAAG GATCTTACCG 5750
CTGTTGAGAT CCAGTTGGAT GTAAOCCACT CGTGCAOCCA ACTGATCTTC 5800
AGCATCTTTT ACTTTCACCA GCGTTTCTGG GTGAGCAAAA ACAGGAAGGC 5850
AAAATGCCGC AAAAAGGGA ATAAGGCGCA CACGGAATG TTGAATACTC 5900
ATACTCTTCC TTTTTCATA TTATTGAAGC ATTTATCAGG GTTATTGTCT 5950
CATGAGCGGA TACATATTG AATGTATTTA GAAAAATATA CAAATAGGGG 6000
TTCCGCGCAC ATTTCCCGCA AAAGTGCCAC CTGACGCTTA AGAAACCAAT 6050
ATTATCATGA CATTAAOCTA TAAAAATAGG CGTATCACGA GGCCCTTTTG 6100
TCTTCAAGAA TTCTCATGTT TGACAGCTTA TCGTAGACAT CATCGTGCT 6150
GTTGGTGTTT TTCTGGOCAT CTGTCTGTG ACCATTTTG TCTCTCCAAC 6200
ATGGGGCAAT TGGCATACC CATGTTGTCA CGTCACTCAG CTCCGCGCTC 6250
AACACCTTCT CGGTTGGAA AACATTAGCG ACATTTACCT GGTGAGCAAT 6300
CAGACATGCG ACGGCTTTAG CCTGGCCTCC TTAATTCAC CTAAGAAATG 6350

GAGCAACCAG CAGGAARAG ACAAGCAGCG AAAATTCAAG CCCCCTGGG 6400
AGGTGCGCGC ATATGCBAAG GATAGCACTC CCACTCTACT ACTGGGTATC 6450
ATATGCTGAC TGTATATGCA TGAGGATAGC ATATGCTACC CGGATACAGA 6500
TTAGGATAGC ATATACTACC CAGATATAGA TTAGGATAGC ATATGCTACC 6550
CAGATATAGA TTAGGATAGC CTATGCTACC CAGATATAAA TTAGGATAGC 6600
ATATACTACC CAGATATAGA TTAGGATAGC ATATGCTACC CAGATATAGA 6650
TTAGGATAGC CTATGCTACC CAGATATAGA TTAGGATAGC ATATGCTACC 6700
CAGATATAGA TTAGGATAGC ATATGCTATC CAGATATTGG GGTAGTATAT 6750
GCTACCCAGA TATAAATTAG GATAGCATAT ACTACCOCTAA TCCTATTAG 6800
GATAGCATAT GCTACCCGGA TACAGATTAG GATAGCATAT ACTACCCAGA 6850
TATAGATTAG GATAGCATAT GCTACCCAGA TATAGATTAG GATAGCCTAT 6900
GCTACCCAGA TATAAATTAG GATAGCATAT ACTACCCAGA TATAGATTAG 6950
GATAGCATAT GCTACCCAGA TATAGATTAG GATAGCCTAT GCTACCCAGA 7000
TATAGATTAG GATAGCATAT GCTACCCAGA TATTGGGTA GTATATGCTA 7050
CCCATGGCAA CATTAGCCCA CCGTCTCTC AGCGACCTCG TGAATATGAG 7100
GACCAACAAC CCTGTGCTTG GCGCTCAGGC GCAGTGTGT GTAATTGTTC 7150
CTCCAGATCG CAGCAATGCG GCCCTATCTC TGGCCCGCC ACCTACTTAT 7200
GCAGGTATTC CCCGGGTGTC CATTAGTGGT TTTGTGGCA AGTGGTTTGA 7250
CCGCACTGGT TAGCGGGGTT ACAATCAGCC AAGTTATTAC ACCCTTATTT 7300

TACAGTCCAA AACCGCAAGG CGCGTGTGG GGGCTGACGC GTGCCCCAC 7350
TCCACAATTT CAAAAAAG AGTGGCCACT TGTCTTTGTT TATGGGCC 7400
ATTGGCGTGG AGCCCCGTTT AATTTTCGGG GGTGTTAGAG ACAACCACTG 7450
GAGTCGCGTG CTGTCGGCGT CCACTCTCTT TCCCTTGT TCAAAATAGAG 7500
TGTAACAACA TGTTTCACT GTCTTGCTCC CTGCTGGGA CACATCTTAA 7550
TAACCCCACT ATCATATTGC ACTAGGATTA TGTGTTGCC ATAGCCATAA 7600
ATTGCTGTGA GATGGACATC CAGTCTTTAC GGTGTTGCC CACCCCATGG 7650
ATTTCATTTG TTAAGATAT TCAGAAATTT TCATTCCTAC ACTAGTATTT 7700
ATTGCCCAAG GGGTTTGTGA GGGTTATATT GGTGTCATAG CACAATGCCA 7750
CCAAGTAAAC CCCGTCCTAA ATTTTATTCT GGGGGGTCA CCTGAAACCT 7800
TGTTTTCGAG CACCTCACAT ACACCTTACT GTTCACAAC CAGCAGTTAT 7850
TCTATTAGCT AAACGAAGGA GAATGAAGAA GCAGGCGAAG ATTCAAGGAG 7900
GTTCAGTACC CTGCTGGAAT CCTGACCCCA TGTAATAAA ACCGTGACAG 8000
CTCATGGGGT GGGAGATATC GCTGTTCTTT AGGACCTTT TACTAACCTT 8050
AATTGGATAG CATATGCTTC CCGTTGGGTA ACATATGCTA TTGAATTAGG 8100
GTTAGTCTGG ATAGTATATA CTAATACCG GGAAGCATAT GCTACCGTT 8150
TAGGGTTAAC AAGGGGGCCT TATAACAACAT ATTGCTAATG CCCTCTTGAG 8200
GTCGCGCTTA TCGGTAGCTA CACAGGCCCC TCTGATTGAC GTTGGTGTAG 8250

2189015

WO 95/29697

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-106-

CCTCCCGTAG TCTTCTGGG CCOCTGGGAG GTACATGTCC CCCAGCATTG 8300
 GTGTAGAGC TTCAGCCAAG AGTTACACAT AAAGGCAATG TTGTGTTGCA 8350
 GTCCACAGAC TGCAAAGTCT GCTCCAGGAT GAAAGCCACT CAGTGTGGC 8400
 AAATGTGCAC ATCCATTAT AAGGATGTCA ACTACAGTCA GAGAACCCCT 8450
 TTGTGTTTGG TCCCCCCCCG TGTACATGT GGAACAGGGC CCAGTTGGCA 8500
 AGTTGTACCA ACCAACTGAA GGGATTACAT GCACTGCCCC 8540

- (2) INFORMATION FOR SEQ ID NO:5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 bases
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (ii) MOLECULE TYPE: Other nucleic acid
 - (A) DESCRIPTION: Oligonucleotide primer UDEC690
 - (iii) HYPOTHETICAL: No
 - (iv) ANTI-SENSE: No
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
- CGCCTGCAGG ACATCCAGAT GACTCAGTCT 30

- (2) INFORMATION FOR SEQ ID NO:6:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 bases
 - (B) TYPE: Nucleic Acid
 - (C) STRANDEDNESS: Single
 - (D) TOPOLOGY: Linear
 - (ii) MOLECULE TYPE: Other nucleic acid

2189015

- (A) DESCRIPTION: Oligonucleotide primer UDEC395
(iii) HYPOTHETICAL: No
(iv) ANTI-SENSE: Yes

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CCCAAGCTTA CTGGATGGTG GGAAGATGGA . 30

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 747 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: Other nucleic acid
(A) DESCRIPTION: 5G1.1M1 scFv (murine)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATG GCC GAC ATC CAG ATG ACT CAG TCT CCA 30
Met Ala Asp Ile Gln Met Thr Gln Ser Pro
1 5 10

GCT TCA CTG TCT GCA TCT GTG GGA GAA ACT 60
Ala Ser Leu Ser Ala Ser Val Gly Glu Thr
15 20

GTC ACC ATC ACA TGT GGA GCA AGT GAG AAT 90
Val Thr Ile Thr Cys Gly Ala Ser Glu Asn
25 30

ATT TAC GGT GCT TTA AAT TGG TAT CAG CGG 120
Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Arg
35 40

AAA CAG GGA AAA TCT CCT CAG CTC CTG ATC 150
 Lys Gln Gly Lys Ser Pro Gln Leu Leu Ile
 45 50

TAT GGT GCA ACC AAC TTG GCA GAT GGC ATG 180
 Tyr Gly Ala Thr Asn Leu Ala Asp Gly Met
 55 60

TCA TCG AGG TTC AGT GGC AGT GGA TCT GGT 210
 Ser Ser Arg Phe Ser Gly Ser Gly Ser Gly
 65 70

AGA CAG TAT TAT CTC AAG ATC AGT AGC CTG 240
 Arg Gln Tyr Tyr Leu Lys Ile Ser Ser Leu
 75 80

CAT CCT GAC GAT GTT GCA ACG TAT TAC TOT 270
 His Pro Asp Asp Val Ala Thr Tyr Tyr Cys
 85 90

CAA AAT GTG TTA AAT ACT CCT CTC ACG TTC 300
 Gln Asn Val Leu Asn Thr Pro Leu Thr Phe
 95 100

GGT GCT GGG ACC AAG TTG GAG CTG AAA CGG 330
 Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg
 105 110

ACC GGA GGT GGC GGG TCG GGT GGC GGG GGA 360
 Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly
 115 120

TCG GGT GGC GGA GGG TCG CAG GTT CAG CTG 390
 Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
 125 130

2189015

CAG CAG TCT GGA GCC GAG CTG ATG AAG CCT 420
Gln Gln Ser Gly Ala Glu Leu Met Lys Pro
135 140

GGG GCC TCA GTG AAG ATG TCC TGC AAG GCT 450
Gly Ala Ser Val Lys Met Ser Cys Lys Ala
145 150

ACT GGC TAC ATA TTC AGT AAC TAC TGG ATA 480
Thr Gly Tyr Ile Phe Ser Asn Tyr Trp Ile
155 160

CAG TGG ATA AAG CAG AGG CCT GGA CAT GGC 510
Gln Trp Ile Lys Gln Arg Pro Gly His Gly
165 170

CTT GAG TGG ATT GGT GAG ATT TTA CCT GGA 540
Leu Glu Trp Ile Gly Glu Ile Leu Pro, Gly
175 180

AGT GGT TCT ACT GAG TAC ACT GAG AAC TTC 570
Ser Gly Ser Thr Glu, Tyr Thr Glu Asn Phe
185 190

AAG GAC AAG GCC GCA TTC ACT GCA GAT ACA 600
Lys Asp Lys Ala Ala Phe Thr Ala Asp Thr
195 200

TCC TCC AAC ACA GCC TAC ATG CAA CTC AGC 630
Ser Ser Asn Thr Ala Tyr Met Gln Leu Ser
205 210

AGC CTG ACA TCA GAG GAC TCT GCC GTC TAT 660
Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr
215 220

- 110 -

TAC TGT GCA AGA TAT TTC TTC GGT AGT AGC 690
Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser
225 230

CCC AAC TGG TAC TTC GAT GTC TGG GGC GCA 720
Pro Asn Trp Tyr Phe Asp Val Trp Gly Ala
235 240

GGG ACC ACG GTC ACC GTC TCC TCA TGA 747
Gly Thr Thr Val Thr Val Ser Ser
245

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 747 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: 5g1.1 scFv CB (humanized)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATG GCC GAT ATC CAG ATG ACC CAG TCC CCG 30
Met Ala Asp Ile Gln Met Thr Gln Ser Pro
1 5 10

TCC TCC CTG TCC GCC TCT GTG GGC GAT AGG 60
Ser Ser Leu Ser Ala Ser Val Gly Asp Arg
15 20

GTC ACC ATC ACC TGC GGC GCC AGC GAA AAC 90
Val Thr Ile Thr Cys Gly Ala Ser Glu Asn
25 30

- 111 -

2189015

ATC TAT GGC GCG CTG AAC TGG TAT CAA CGT 120
Ile Tyr Gly Ala Leu Asn Trp Tyr Gln Arg
35 40

AAA CCT GGG AAA GCT CCG AAG CTT CTG ATT 150
Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
45 50

TAC GGT GCG ACG AAC CTG GCA GAT GGA GTC 180
Tyr Gly Ala Thr Asn Leu Ala Asp Gly Val
55 60

CCT TCT CGC TTC TCT GGA TCC GGC TCC GGA 210
Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly
65 70

ACG GAT TTC ACT CTG ACC ATC AGC AGT CTG 240
Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu
75 80

CAG CCT GAA GAC TTC GCT ACG TAT TAC TGT 270
Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys
85 90

CAG AAC GTT TTA AAT ACT CCG TTG ACT TTC 300
Gln Asn Val Leu Asn Thr Pro Leu Thr Phe
95 100

GGA CAG GGT ACC AAG GTG GAA ATA AAA CGT 330
Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
105 110

ACT GGC GGT GGT GGT TCT GGT GGC GGT GGA 360
Thr Gly Gly Gly Gly Ser Gly Gly Gly Gly
115 120

- 112 -

TCT GGT GGT GGC GGT TCT CAA GTC CAA CTG 390
Ser Gly Gly Gly Gly Ser Gln Val Gln Leu
125 130

GTC CAA TCC GGC GCC GAG GTC AAG AAG CCA 420
Val Gln Ser Gly Ala Glu Val Lys Lys Pro
135 140

GGG GCC TCA GTC AAA GTG TCC TGT AAA GCT 450
Gly Ala Ser Val Lys Val Ser Cys Lys Ala
145 150

AGC GGC TAT ATT TTT TCT AAT TAT TGG ATT 480
Ser Gly Tyr Ile Phe Ser Asn Tyr Trp Ile
155 160

CAA TGG GTG CGT CAG GCC CCC GGG CAG GGC 510
Gln Trp Val Arg Gln Ala Pro Gly Gln Gly
165 170

CTG GAA TGG ATG GGT GAG ATC TTA CCG GGC 540
Leu Glu Trp Met Gly Glu Ile Leu Phe Gly
175 180

TCT GGT AGC ACC GAA TAT ACC GAA AAT TTT 570
Ser Gly Ser Thr Glu Tyr Thr Glu Asn Phe
185 190

AAA GAC CGT GTT ACT ATG ACG CGT GAC ACT 600
Lys Asp Arg Val Thr Met Thr Arg Asp Thr
195 200

TGG ACT AGT ACA GTA TAC ATG GAG CTC TCC 630
Ser Thr Ser Thr Val Tyr Met Glu Leu Ser
205 210

- 113 -

2189015

AGC CTG CGA TCG GAG GAC ACG GCC GTC TAT 660
Ser Leu Arg Ser Glu Asp Thr Ala Val Tyr
215 220

TAT TGC GCG CGT TAT TTT TTT GGT TCT AGC 690
Tyr Cys Ala Arg Tyr Phe Phe Gly Ser Ser
225 230

CCG AAT TGG TAT TTT GAT GTT TGG GGT CAA 720
Pro Asn Trp Tyr Phe Asp Val Trp Gly Gln
235 240

GGA ACC CTG GTC ACT GTC TCG AGC TGA 747
Gly Thr Leu Val Thr Val Ser Ser
245

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 726 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

(A) DESCRIPTION: 5G1.1M1 VL HuK (chimeric light chain)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG GGA ATC CAA GGA GGG TCT GTC CTG TTC 30
Met Gly Ile Gln Gly Gly Ser Val Leu Phe
-25 -20

GGG CTG CTG CTC GTC CTG GCT GTC TTC TGC 60
Gly Leu Leu Leu Val Leu Ala Val Phe Cys
-15 -10

- 114 -

CAT TCA GGT CAT AGC CTG CAG GAC ATC CAG 90
 His Ser Gly His Ser Leu Gln Asp Ile Gln
 -5 1 5

ATG ACT CAG TCT CCA GCT TCA CTG TCT GCA 120
 Met Thr Gln Ser Pro Ala Ser Leu Ser Ala
 10 15

TCT GTG GGA GAA ACT GTC ACC ATC ACA TGT 150
 Ser Val Gly Glu Thr Val Thr Ile Thr Cys
 20 25

GGA GCA AGT GAG AAT ATT TAC GGT GCT TTA 180
 Gly Ala Ser Glu Asn Ile Tyr Gly Ala Leu
 30 35

AAT TGG TAT CAG CGG AAA CAG GGA AAA TCT 210
 Asn Trp Tyr Gln Arg Lys Gln Gly Lys Ser
 40 45

CCT CAG CTC CTG ATC TAT GGT GCA ACC AAC 240
 Pro Gln Leu Leu Ile Tyr Gly Ala Thr Asn
 50 55

TTG GCA GAT GGC ATG TCA TCG AGG TTC AGT 270
 Leu Ala Asp Gly Met Ser Ser Arg Phe Ser
 60 65

GGC AGT GGA TCT GGT AGA CAG TAT TAT CTC 300
 Gly Ser Gly Ser Gly Arg Gln Tyr Tyr Leu
 70 75

AAG ATC AGT AGC CTG CAT CCT GAC GAT GTT 330
 Lys Ile Ser Ser Leu His Pro Asp Asp Val
 80 85

2189015

- 115 -

GCA ACG TAT TAC TGT CAA AAT GTG TTA AAT 360
Ala Thr Tyr Tyr Cys Gln Asn Val Leu Asn
90 95

ACT CCT CTC ACG TTC GGT GCT GGG ACC AAG 390
Thr Pro Leu Thr Phe Gly Ala Gly Thr Lys
100 105

TIG GAG CTG AAA CGA ACT GTG GCT GCA CCA 420
Leu Glu Leu Lys Arg Thr Val Ala Ala Pro
110 115

TCT GTC TTC ATC TTC CCG CCA TCT GAT GAG 450
Ser Val Phe Ile Phe Pro Pro Ser Asp Glu
120 125

CAG TIG AAA TCT GGA ACT GCC TCT GTT GTG 480
Gln Leu Lys Ser Gly Thr Ala Ser Val Val
130 135

TGC CTG CTG AAT AAC TTC TAT CCC AGA GAG 510
Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu
140 145

GCC AAA GTA CAG TGG AAG GTG GAT AAC GCC 540
Ala Lys Val Gln Trp Lys Val Asp Asn Ala
150 155

CTC CAA TCG GGT AAC TCC CAG GAG AGT GTC 570
Leu Gln Ser Gly Asn Ser Gln Glu Ser Val
160 165

ACA GAG CAG GAC AGC AAG GAC AGC ACC TAC 600
Thr Glu Gln Asp Ser Lys Asp Ser Thr Tyr
170 175

- 116 -

AGC CTC AGC AGC ACC CTG ACG CTG AGC AAA 630
 Ser Leu Ser Ser Thr Leu Thr Leu Ser Lys
 180 185

GCA GAC TAC GAG AAA CAC AAA GTC TAC GCC 660
 Ala Asp Tyr Glu Lys His Lys Val Tyr Ala
 190 195

TGC GAA GTC ACC CAT CAG GGC CTG AGC TCG 690
 Cys Glu Val Thr His Gln Gly Leu Ser Ser
 200 205

CCC GTC ACA AAG AGC TTC AAC AGG GGA GAG 720
 Pro Val Thr Lys Ser Phe Asn Arg Gly Glu
 210 215

TGT TAG 726
 Cys

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1M1 VH +HuG1 (chimeric Fd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

ATG AAA TGG AGC TGG GTT ATT CTC TTC CTC 30
 Met Lys Trp Ser Trp Val Ile Leu Phe Leu
 -15 -10

CTG TCA GTA ACT GCA GGT GTC CAC TCC CAG 60
 Leu Ser Val Thr Ala Gly Val His Ser Gln
 -5 1

2189015

GTT CAG CTG CAG CAG TCT GGA GCT GAG CTG 90
Val Gln Leu Gln Gln Ser Gly Ala Glu Leu
5 10

ATG AAG CCT GGG GCC TCA GTG AAG ATG TCC 120
Met Lys Pro Gly Ala Ser Val Lys Met Ser
15 20

TGC AAG GCT ACT GGC TAC ATA TTC AGT AAC 150
Cys Lys Ala Thr Gly Tyr Ile Phe Ser Asn
25 30

TAC TGG ATA CAG TGG ATA AAG CAG AGG CCT 180
Tyr Trp Ile Gln Trp Ile Lys Gln Arg Pro
35 40

GGA CAT GGC CTT GAG TGG ATT GGT GAG ATT 210
Gly His Gly Leu Glu Trp Ile Gly Glu Ile
45 50

TTA CCT GGA AGT GGT TCT ACT GAG TAC ACT 240
Leu Pro Gly Ser Gly Ser Thr Glu Tyr Thr
55 60

GAG AAC TTC AAG GAC AAG GCC GCA TTC ACT 270
Glu Asn Phe Lys Asp Lys Ala Ala Phe Thr
65 70

GCA GAT ACA TCC TCC AAC ACA GCC TAC ATG 300
Ala Asp Thr Ser Ser Asn Thr Ala Tyr Met
75 80

CAA CTC AGC AGC CTG ACA TCA GAG GAC TCT 330
Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser
85 90

2189015

WO 95/29697

PCT/US95/05688

- 118 -

GCC GTC TAT TAC TGT GCA AGA TAT TTC TTC 360
Ala Val Tyr Tyr Cys Ala Arg Tyr Phe Phe
95 100

GGT AGT AGC CCC AAC TGG TAC TTC GAT GTC 390
Gly Ser Ser Pro Asn Trp Tyr Phe Asp Val
105 110

TGG GGC GCA GGG ACC ACG GTC ACC GTC TCC 420
Trp Gly Ala Gly Thr Thr Val Thr Val Ser
115 120

TCA GCC TCC ACC AAG GGC CCA TGG GTC TTC 450
Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
125 130

CCC CTG GCG CCC TGC TCC AAG AGC ACC TCT 480
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
135 140

GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC 510
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
145 150

AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG 540
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
155 160

TGG TGG AAC TCA GGC GCC CTG ACC AGC GGC 570
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
165 170

GTG CAC ACC TTC CCG GGT GTC CTA CAG TCC 600
Val His Thr Phe Pro Ala Val Leu Gln Ser
175 180

- 119 -

2189015

TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG 630
 Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
 185 190

ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG 660
 Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
 195 200

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC 690
 Thr Tyr Ile Cys Asn Val Asn His Lys Pro
 205 210

AGC AAC ACC AAG GTG GAC AAG AAA GTC GAG 720
 Ser Asn Thr Lys Val Asp Lys Lys Val Glu
 215 220

CCC AAA TCT TGT GAC AAA ACT CAC ACA TAA 750
 Pro Lys Ser Cys Asp Lys Thr His Thr
 225

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5g1.1 VH + IGHL (Humanized Fd)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATG AAG TGG AGC TGG GTT ATT CTC TTC CTC 30
 Met Lys Trp Ser Trp Val Ile Leu Phe Leu

- 120 -

CTG TCA GTA ACT GCC GGC GTC CAC TCC CAA 60
Leu Ser Val Thr Ala Gly Val His Ser Gln
-5 1

GTC CAA CTG GTG CAA TCC GGC GCC GAG GTC 90
Val Gln Leu Val Gln Ser Gly Ala Glu Val
5 10

AAG AAG CCA GGG GCC TCA GTC AAA GTG TCC 120
Lys Lys Pro Gly Ala Ser Val Lys Val Ser
15 20

TGT AAA GCT AGC GGC TAT ATT TTT TCT AAT 150
Cys Lys Ala Ser Gly Tyr Ile Phe Ser Asn
25 30

TAT TGG ATT CAA TGG GTG CGT CAG GCC CCC 180
Tyr Trp Ile Gln Trp Val Arg Gln Ala Pro
35 40

GGG CAG GGC CTG GAA TGG ATG GGT GAG ATC 210
Gly Gln Gly Leu Glu Trp Met Gly Glu Ile
45 50

TTA CCG GGC TCT GGT AGC ACC GAA TAT GCC 240
Leu Pro Gly Ser Gly Ser Thr Glu Tyr Ala
55 60

CAA AAA TTC CAG GGC CGT GTT ACT ATG ACT 270
Gln Lys Phe Gln Gly Arg Val Thr Met Thr
65 70

GCG GAC ACT TCG ACT AGT ACA GGC TAC ATG 300
Ala Asp Thr Ser Thr Ser Thr Ala Tyr Met
75 80

GAG CTC TCC AGC CTG CGA TCG GAG GAC ACG 330
Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
85 90

GCC GTC TAT TAT TGC GCG CGT TAT TTT TTT 360
Ala Val Tyr Tyr Cys Ala Arg Tyr Phe Phe
95 100

GGT TCT AGC CCG AAT TGG TAT TTT GAT GTT 390
Gly Ser Ser Pro Asn Trp Tyr Phe Asp Val
105 110

TGG GGT CAA GGA ACC CTG GTC ACT GTC TCG 420
Trp Gly Gln Gly Thr Leu Val Thr Val Ser
115 120

AGC GCC TCC ACC AAG GGC CCA TCG GTC TTC 450
Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
125 130

CCC CTG GCG CCC TCC TCC AAG AGC ACC TCT 480
Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
135 140

GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC 510
Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
145 150

AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG 540
Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
155 160

TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC 570
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
165 170

- 122 -

GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC 600
Val His Thr Phe Pro Ala Val Leu Gln Ser
175 180

TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG 630
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
185 190

ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG 660
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
195 200

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC 690
Thr Tyr Ile Cys Asn Val Asn His Lys Pro
205 210

AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG 720
Ser Asn Thr Lys Val Asp Lys Lys Val Glu
215 220

CCC AAA TCT TGT GAC AAA ACT CAC ACA TAA 750
Pro Lys Ser Cys Asp Lys Thr His Thr
225 230

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 750 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1 VH + IGHRLC (Humanized Fd)

2189015

- 123 -

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

ATG AAG TGG AGC TGG GTT ATT CTC TTC CTC 30
Met Lys Trp Ser Trp Val Ile Leu Phe Leu
-15 -10

CTG TCA GTA ACT GGC GGC GTC CAC TCC CAA 60
Leu Ser Val Thr Ala Gly Val His Ser Gln
-5 1

GTC CAA CTG GTG CAA TCC GGC GCC GAG GTC 90
Val Gln Leu Val Gln Ser Gly Ala Glu Val
5 10

AAG AAG CCA GGG GCC TCA GTC AAA GTG TCC 120
Lys Lys Pro Gly Ala Ser Val Lys Val Ser
15 20

TGT AAA GCT AGC GGC TAT ATT TTT TCT AAT 150
Cys Lys Ala Ser Gly Tyr Ile Phe Ser Asn
25 30

TAT TGG ATT CAA TGG GTG CGT CAG GCC CCC 180
Tyr Trp Ile Gln Trp Val Arg Gln Ala Pro
35 40

GGG CAG GGC CTG GAA TGG ATG GGT GAG ATC 210
Gly Gln Gly Leu Glu Trp Met Gly Glu Ile
45 50

TTA CCG GGC TCT GGT AGC ACC GAA TAT ACC 240
Leu Pro Gly Ser Gly Ser Thr Glu Tyr Thr
55 60

GAA AAT TTT AAA GAC CGT GTT ACT ATG ACG 270
Glu Asn Phe Lys Asp Arg Val Thr Met Thr
65 70

- 124 -

CGT GAC ACT TCG ACT AGT ACA GTA TAC ATG 300
 Arg Asp Thr Ser Thr Ser Thr Val Tyr Met
 75 80

GAG CTC TCC AGC CTG CGA TCG GAG GAC ACG 330
 Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr
 85 90

GCC GTC TAT TAT TGC GCG CGT TAT TTT TTT 360
 Ala Val Tyr Tyr Cys Ala Arg Tyr Phe Phe
 95 100

GGT TCT AGC CCG AAT TGG TAT TTT GAT GTT 390
 Gly Ser Ser Pro Asn Trp Tyr Phe Asp Val
 105 110

TGG GGT CAA GGA ACC CTG GTC ACT GTC TCG 420
 Trp Gly Gln Gly Thr Leu Val Thr Val Ser
 115 120

AGC GCC TCC ACC AAG GGC CCA TCG GTC TTC 450
 Ser Ala Ser Thr Lys Gly Pro Ser Val Phe
 125 130

CCC CTG GCG CCC TCC TCC AAG AGC ACC TCT 480
 Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser
 135 140

GGG GGC ACA GCG GCC CTG GGC TGC CTG GTC 510
 Gly Gly Thr Ala Ala Leu Gly Cys Leu Val
 145 150

AAG GAC TAC TTC CCC GAA CCG GTG ACG GTG 540
 Lys Asp Tyr Phe Pro Glu Pro Val Thr Val
 155 160

- 125 -

2189015

TCG TGG AAC TCA GGC GCC CTG ACC AGC GGC 570
Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly
165 170

GTG CAC ACC TTC CCG GCT GTC CTA CAG TCC 600
Val His Thr Phe Pro Ala Val Leu Gln Ser
175 180

TCA GGA CTC TAC TCC CTC AGC AGC GTG GTG 630
Ser Gly Leu Tyr Ser Leu Ser Ser Val Val
185 190

ACC GTG CCC TCC AGC AGC TTG GGC ACC CAG 660
Thr Val Pro Ser Ser Ser Leu Gly Thr Gln
195 200

ACC TAC ATC TGC AAC GTG AAT CAC AAG CCC 690
Thr Tyr Ile Cys Asn Val Asn His Lys Pro
205 210

AGC AAC ACC AAG GTG GAC AAG AAA GTT GAG 720
Ser Asn Thr Lys Val Asp Lys Lys Val Glu
215 220

CCC AAA TCT TGT GAC AAA ACT CAC ACA TAA 750
Pro Lys Ser Cys Asp Lys Thr His Thr
225 230

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: Nucleic Acid
- (C) STRANDEDNESS: Double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other nucleic acid

- (A) DESCRIPTION: 5G1.1 VL +KLV56

(Rumanized light chain)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

ATG GGA ATC CAA GGA GGG TCT GTC CTG TTC 30
Met Gly Ile Gln Gly Gly Ser Val Leu Phe

-25 -20

GGG CTG CTG CTC GTC CTG GCT GTC TTC TGC 60
Gly Leu Leu Leu Val Leu Ala Val Phe Cys

-15 -10

CAT TCA GGT CAT AGC CTG CAG GAT ATC CAG 90
His Ser Gly His Ser Leu Gln Asp Ile Gln

-5 1 5

ATG ACC CAG TCC CCG TCC TCC CTG TCC GCC 120
Met Thr Gln Ser Pro Ser Ser Leu Ser Ala

10 15

TCT GTG GGC GAT AGG GTC ACC ATC ACC TGC 150
Ser Val Gly Asp Arg Val Thr Ile Thr Cys

20 25

GGC GCC AGC GAA AAC ATC TAT GGC GCG CTG 180
Gly Ala Ser Glu Asn Ile Tyr Gly Ala Leu

30 35

AAC TGG TAT CAA CGT AAA CCT GGG AAA GCT 210
Asn Trp Tyr Gln Arg Lys Pro Gly Lys Ala

40 45

CCG AAG CTT CTG ATT TAC GGT GCG ACG AAC 240
Pro Lys Leu Leu Ile Tyr Gly Ala Thr Asn

50 55

CTG GCA GAT GGA GTC CCT TCT GCG TTC TCT 270
Leu Ala Asp Gly Val Pro Ser Arg Phe Ser

60 65